

STELLER SEA LION GENETICS

Ongoing Studies (Bickham's Lab)

mtDNA Studies

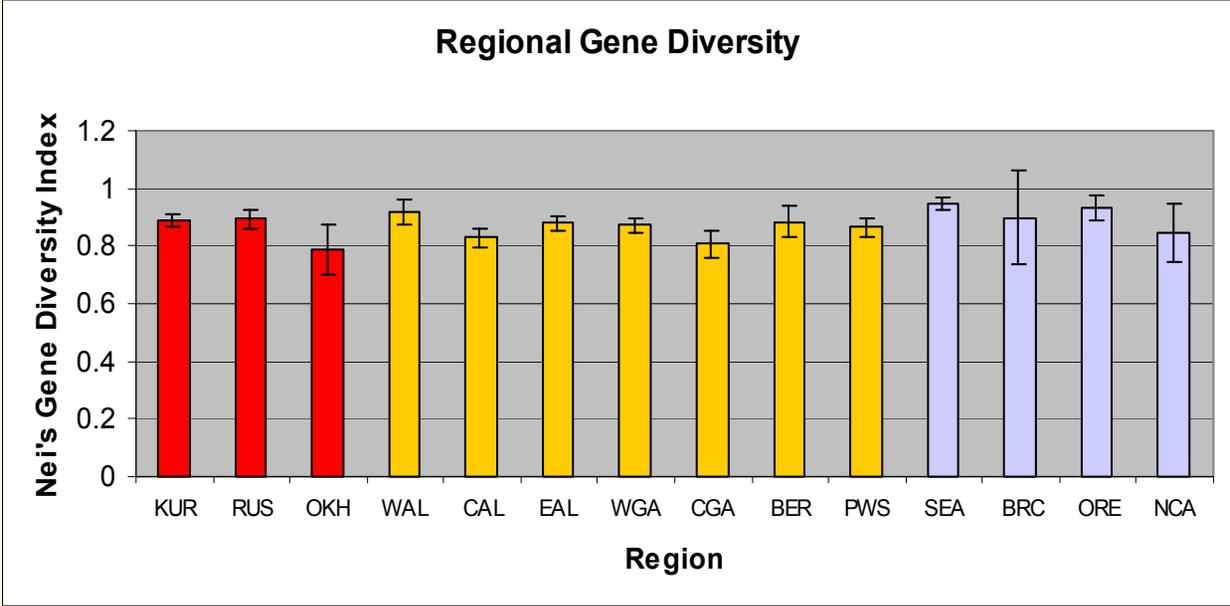
1. Phylogeography and Population Structure based upon control region and Cyt *b* sequences.
2. Origin of the hunter killed animals in the Pribilof Islands.
3. Stock origin and movements of yearlings from Prince William Sound and Southeast Alaska.

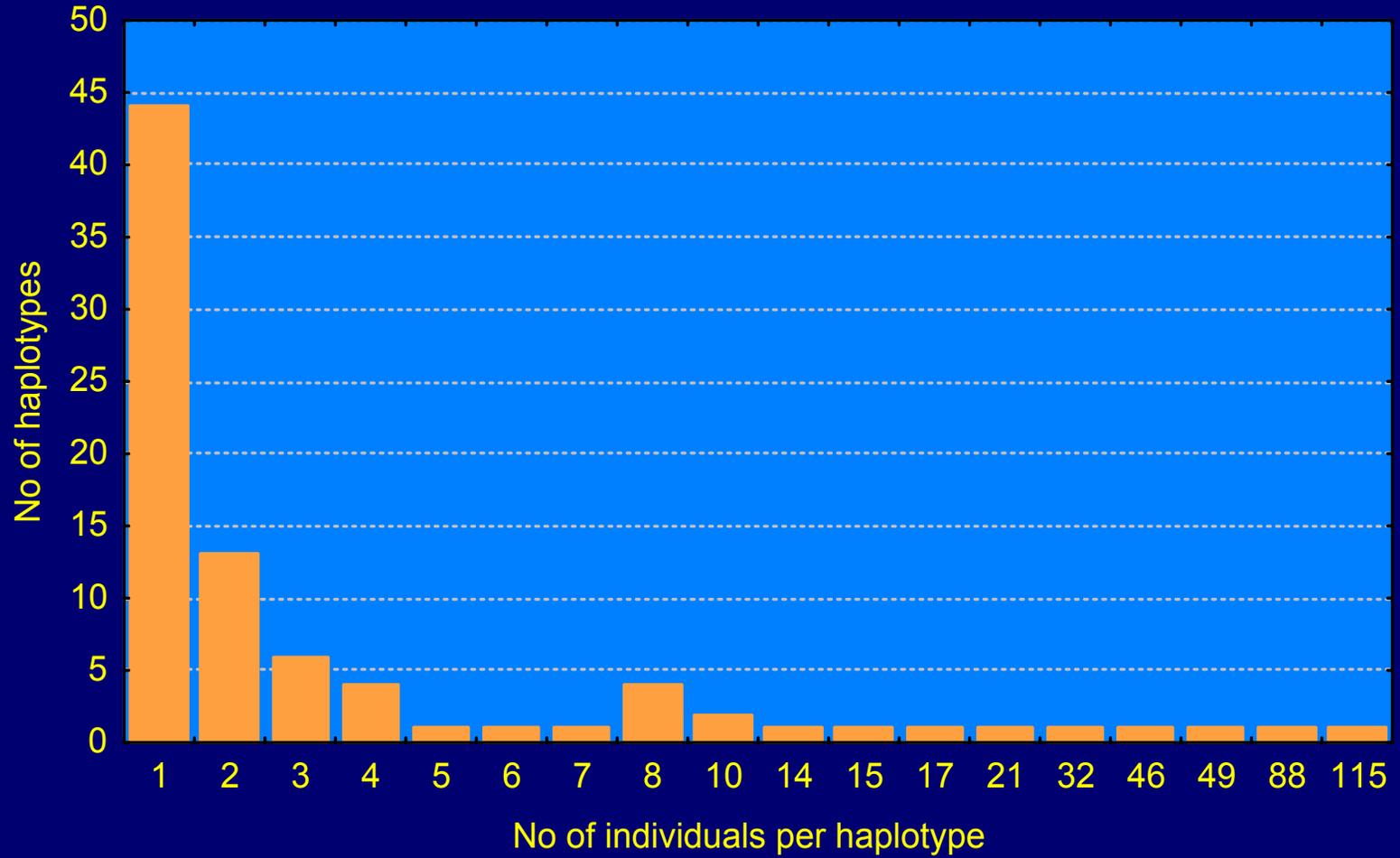
Microsatellite Analyses

1. Geographic survey of rookeries with 6 polymorphic loci.
2. Development and testing of new markers.

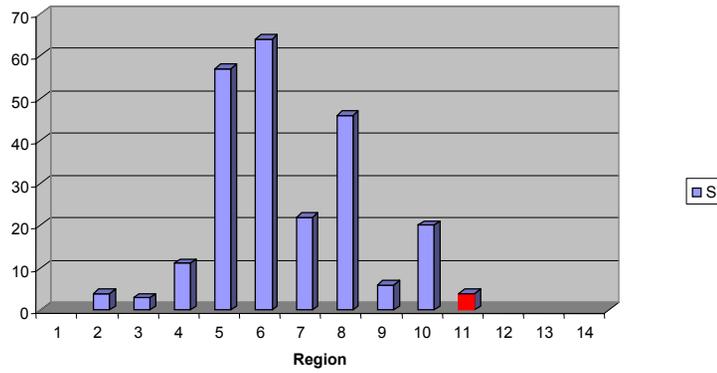
Other nuclear markers

1. Search for variability within X- and Y-chromosome linked markers (Z_{fx}/Z_{fy}).
2. Search for variability within MHC loci.

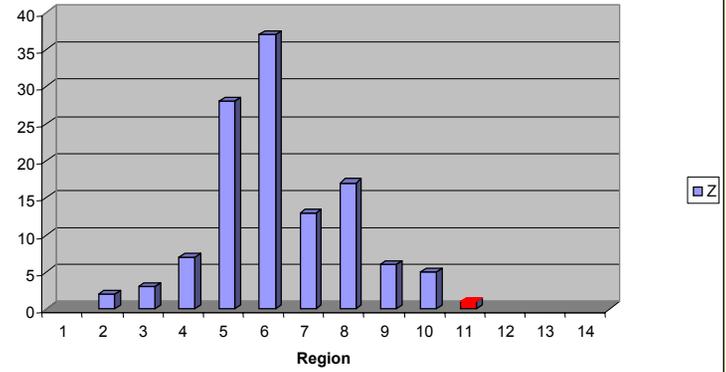




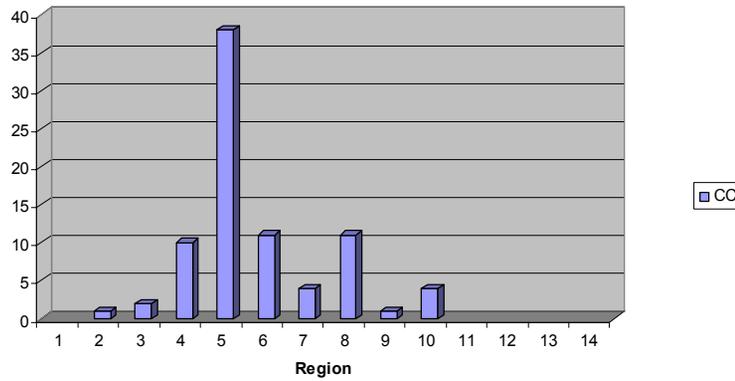
Distribution of haplotype S



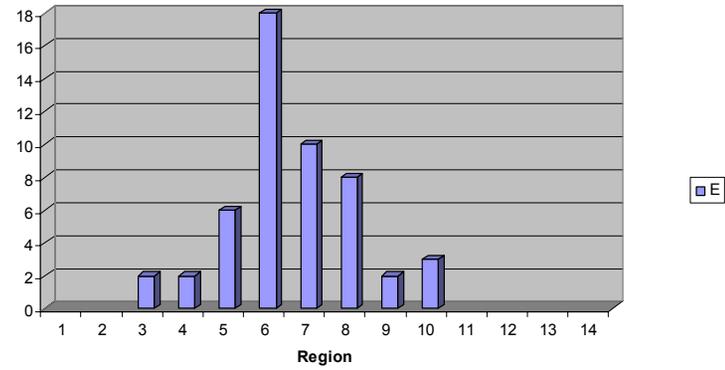
Distribution of haplotype Z



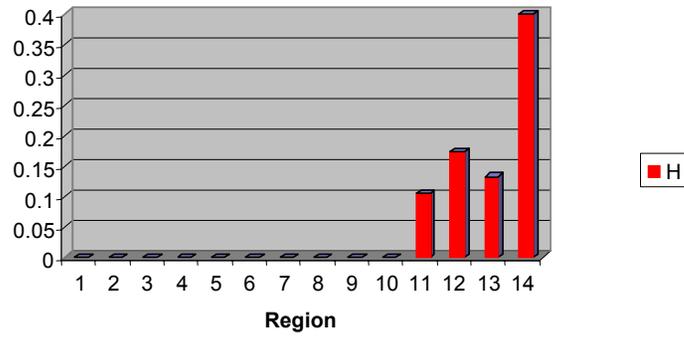
Distribution of haplotype CC



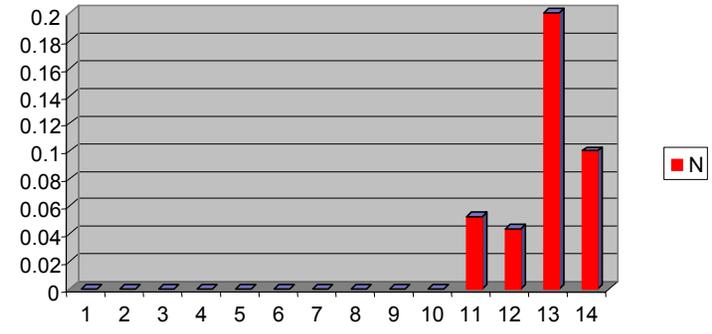
Distribution of haplotype E



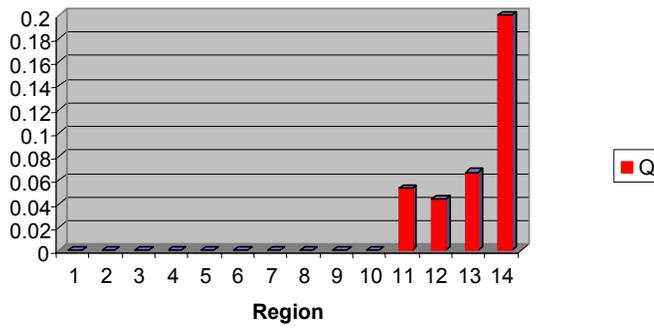
Distribution and Frequencies of haplotype H



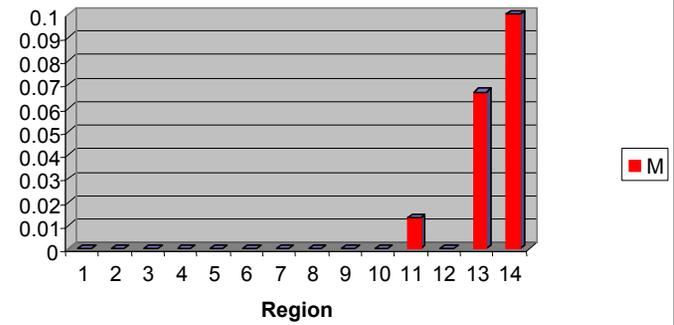
Distribution and Frequencies of haplotype N



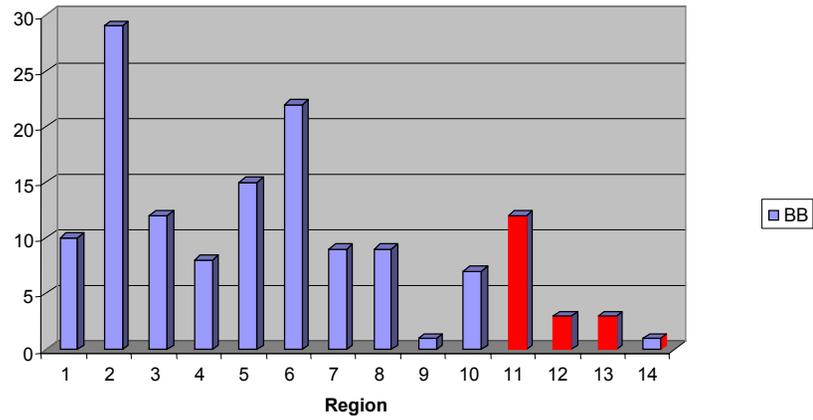
Distribution and Frequencies of haplotype Q



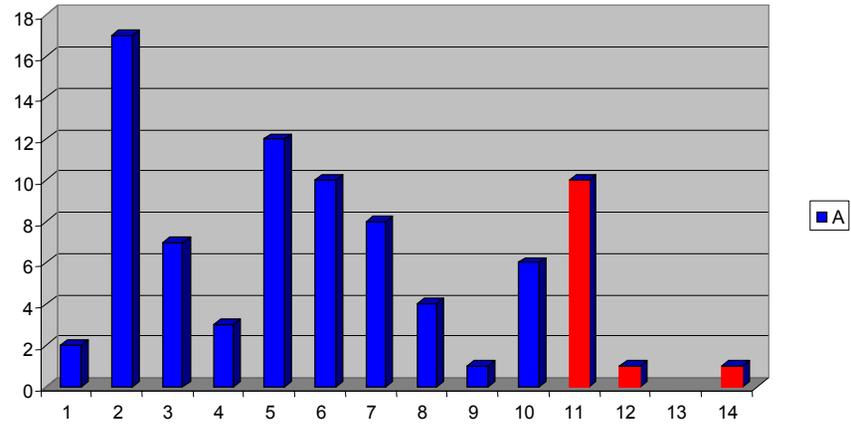
Distribution and Frequencies of haplotype M



Distribution of haplotype BB



Distribution of haplotype A



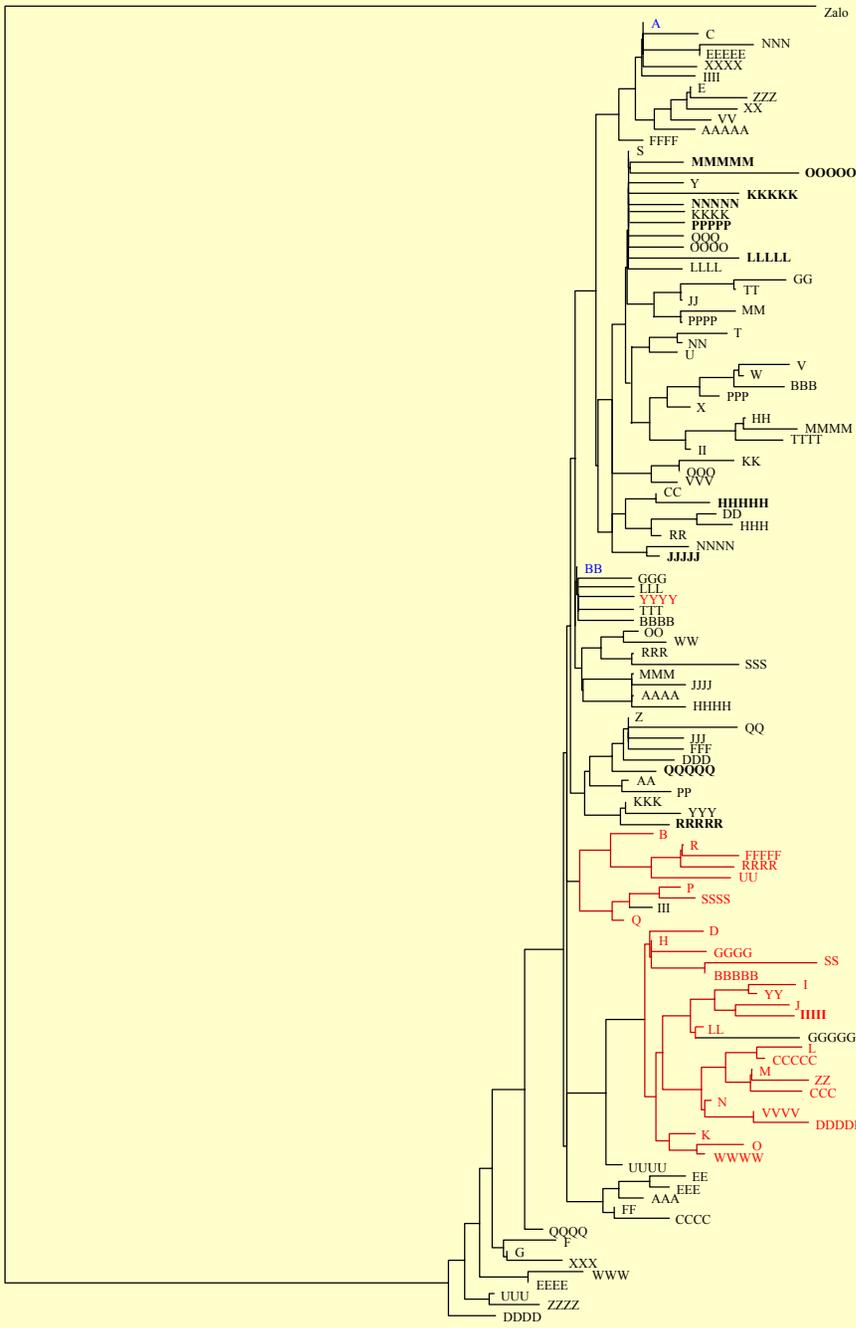


Figure 1.--Neighbor-joining tree of Tamura-Nei distances for 122 mtDNA haplotypes of Steller sea lions. Haplotypes characteristic of the eastern stock are in red, widespread haplotypes are in blue, and haplotypes characteristic of the western stock are in black. New haplotypes are in bold.

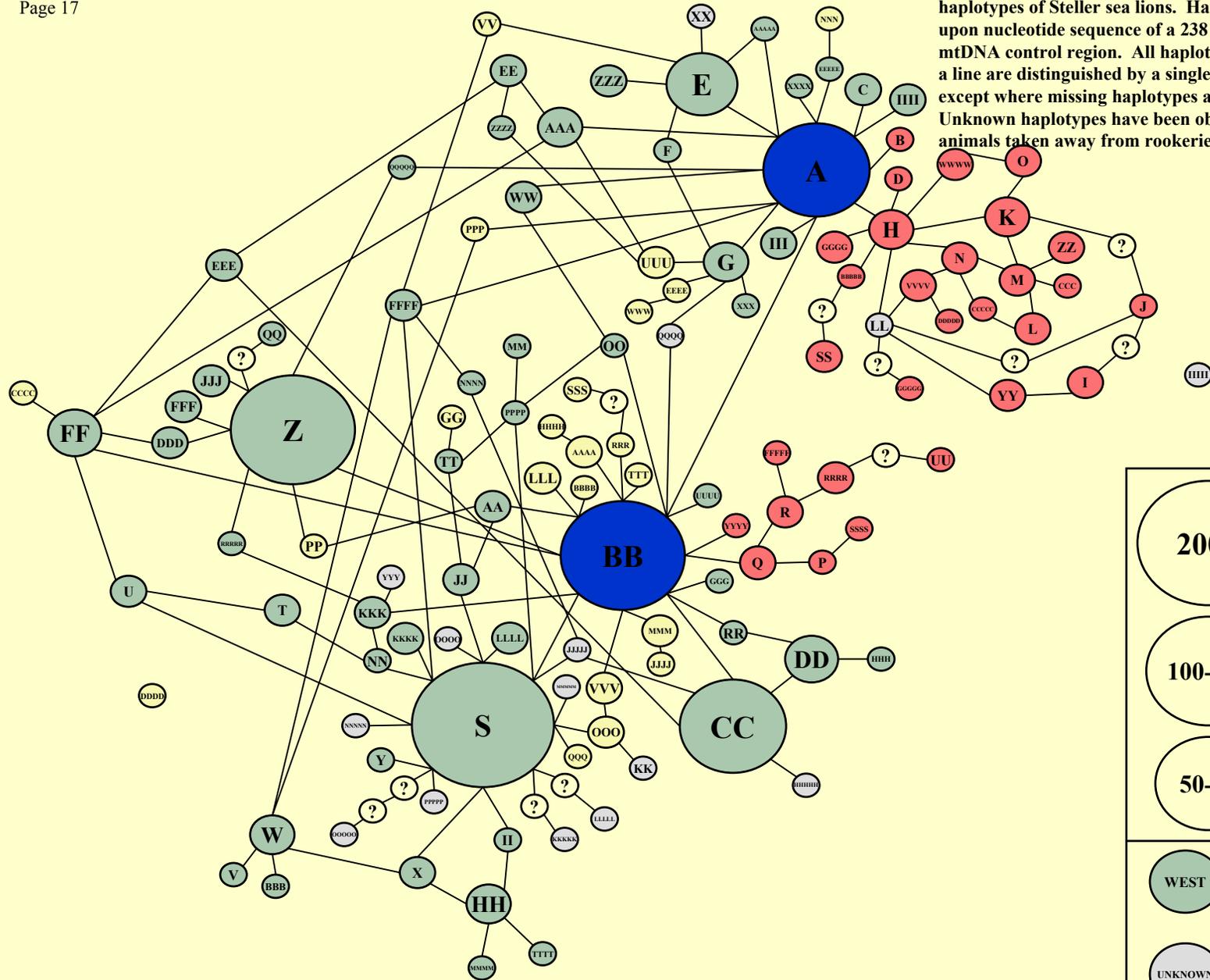
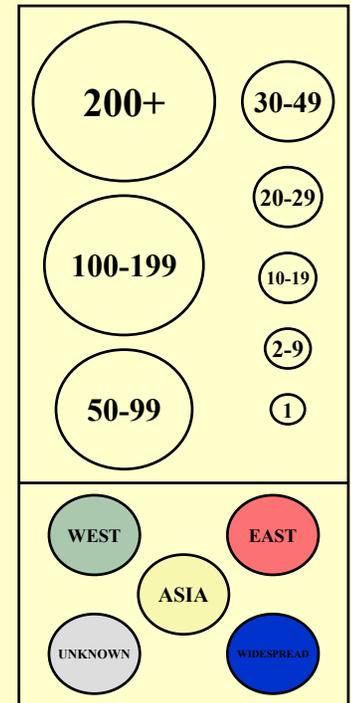


Figure 2.--Minimum spanning network for 122 haplotypes of Steller sea lions. Haplotypes are based upon nucleotide sequence of a 238 bp section of the mtDNA control region. All haplotypes connected by a line are distinguished by a single base pair change except where missing haplotypes are indicated. Unknown haplotypes have been observed only in animals taken away from rookeries.



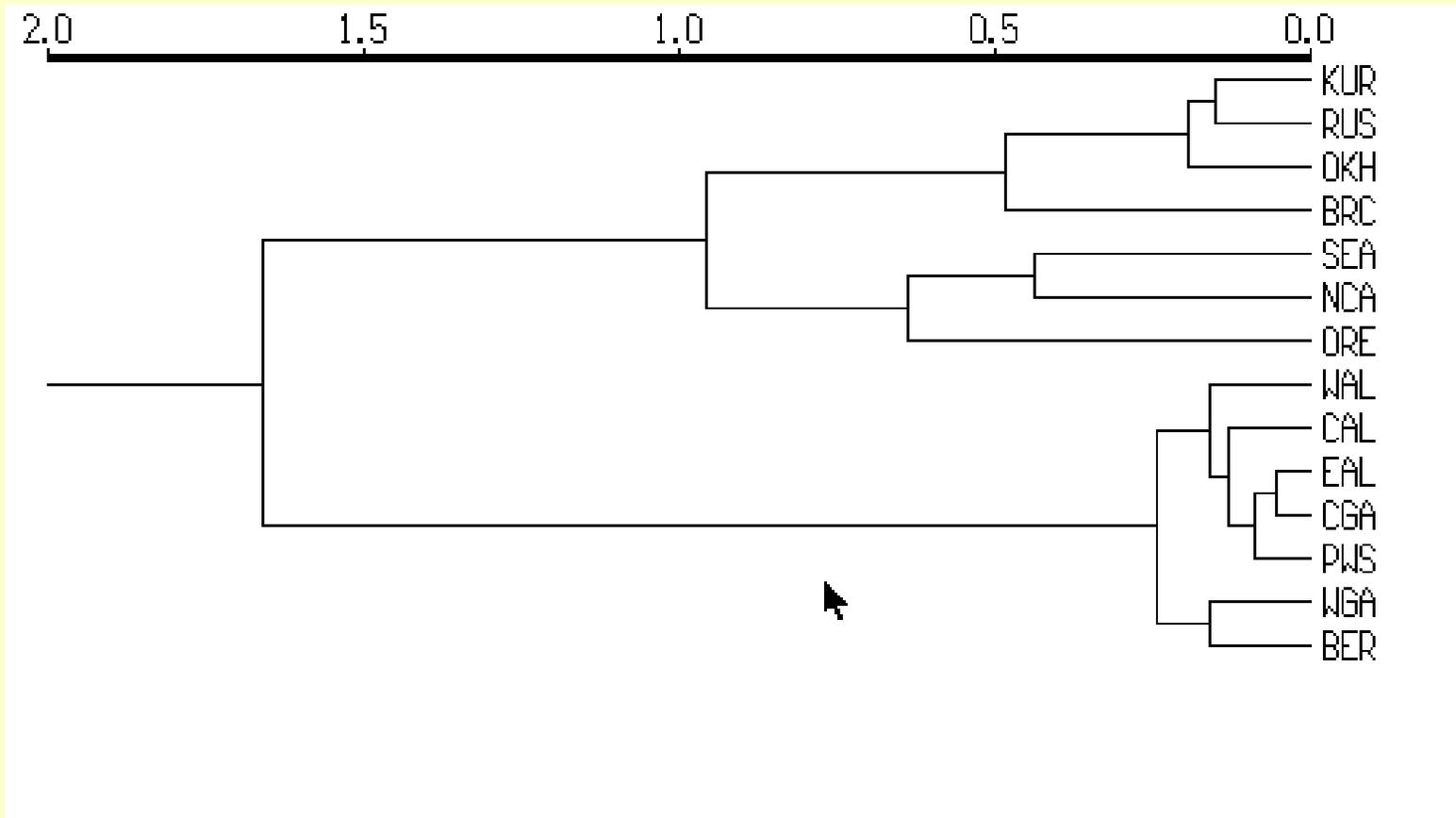


Figure 2.—Cluster analysis of Nei's standard genetic distances for 14 grouped localities of Steller sea lions produced by NTSYS-PC (ver. 1.7). Abbreviations for grouped localities are as in Table 3.

Figure 5.--Neighbor joining tree based upon Slatkin Linearized Fst values showing the relationships among 41 rookeries ($N \geq 10$) of Steller sea lions. Eastern stock rookeries are in red, Asian group western stock rookeries are in blue, and central group western stock rookeries are in black.

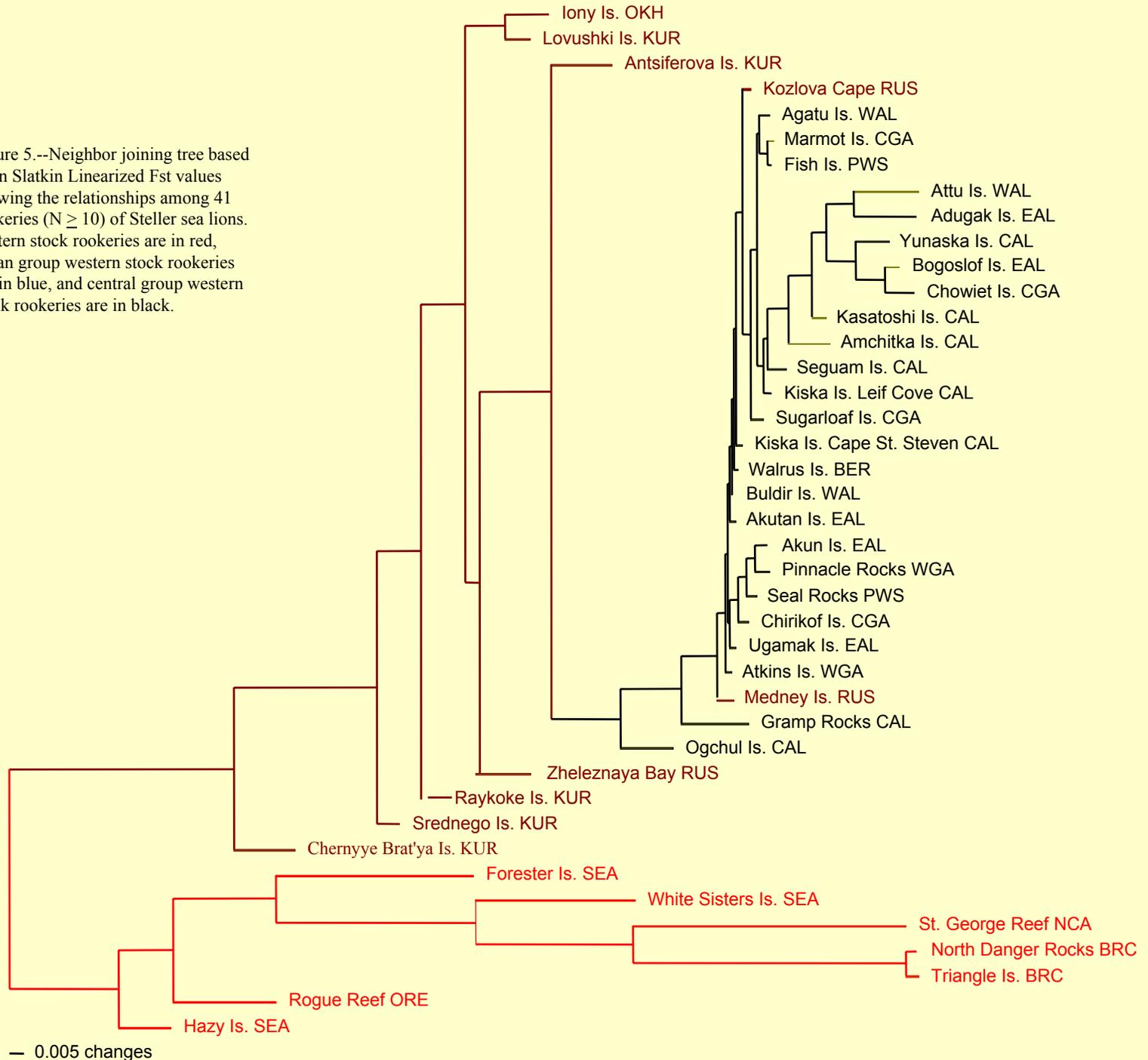
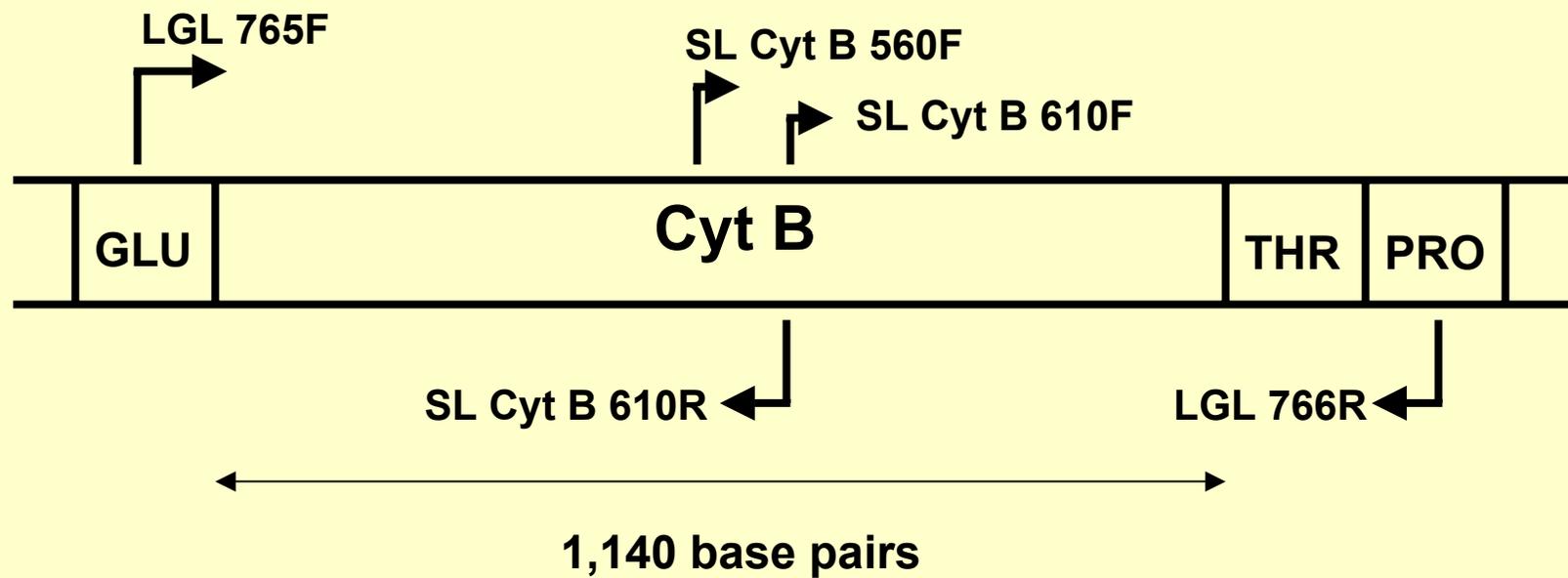


Figure 3.--Map of the cytochrome *b* gene and adjacent tRNAs showing the positions of the PCR and sequencing primers.



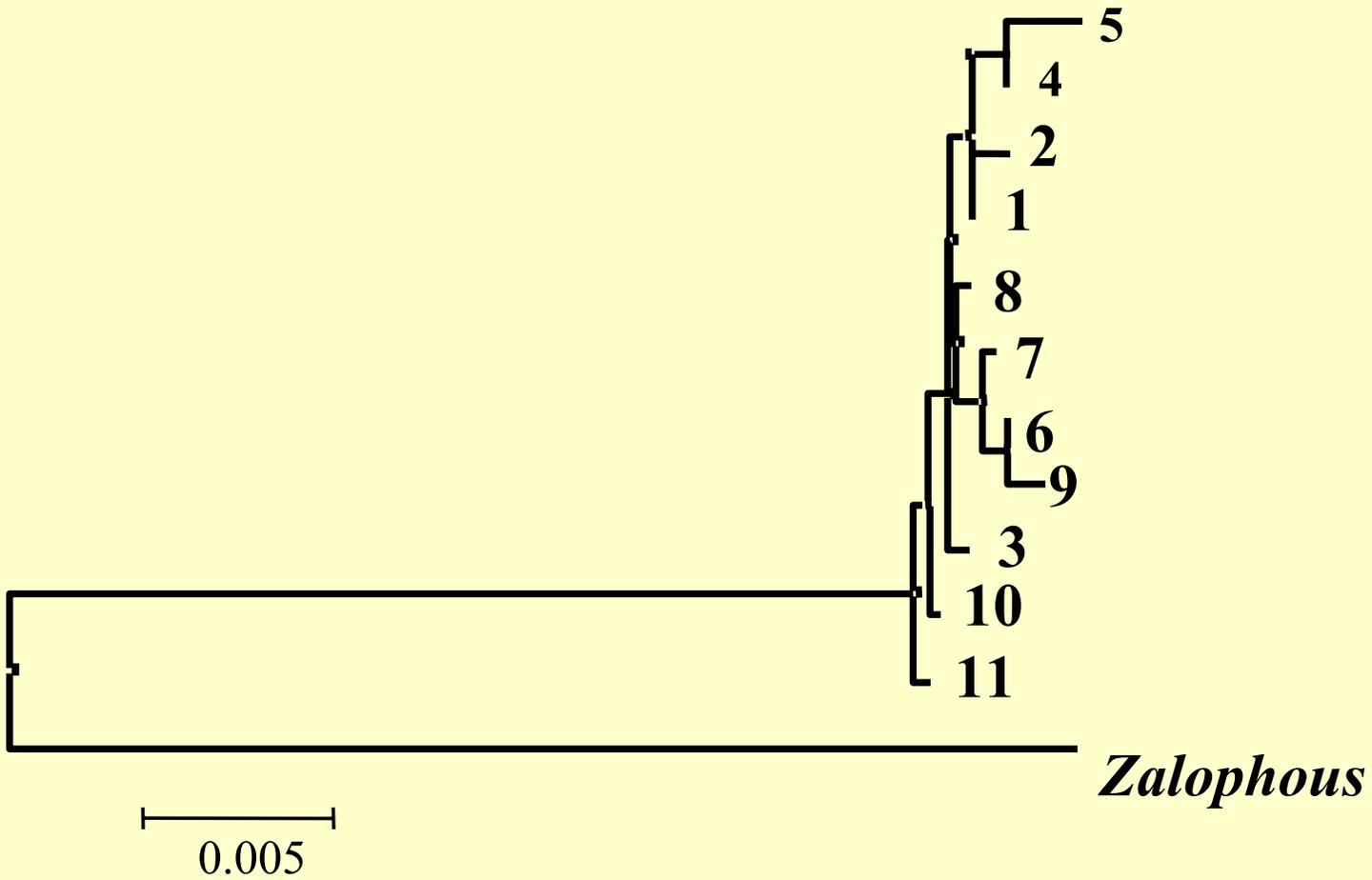
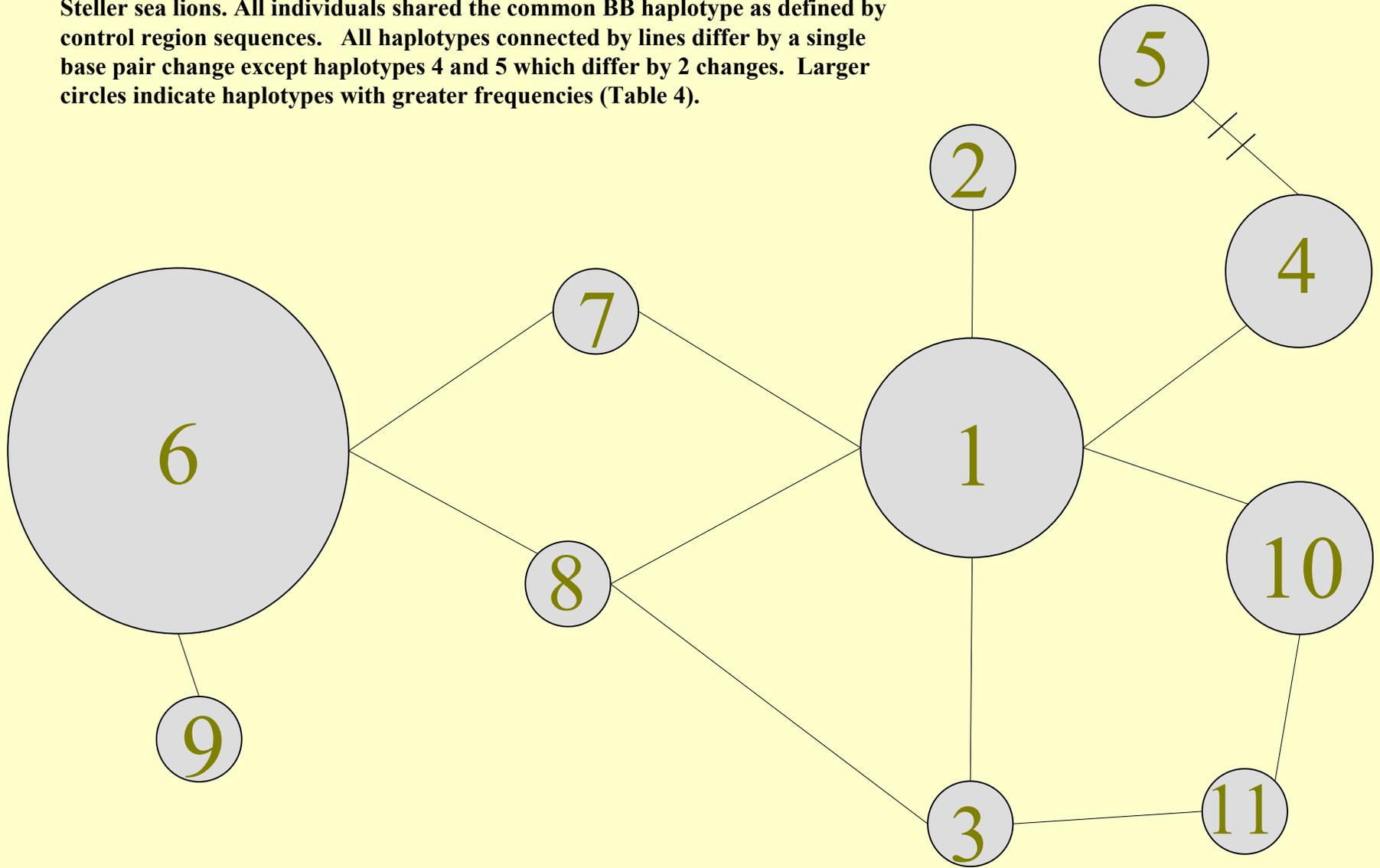


Figure 4.--Minimum spanning network for 11 haplotypes identified by nucleotide sequence analysis of the mitochondrial cytochrome *b* gene of 112 Steller sea lions. All individuals shared the common BB haplotype as defined by control region sequences. All haplotypes connected by lines differ by a single base pair change except haplotypes 4 and 5 which differ by 2 changes. Larger circles indicate haplotypes with greater frequencies (Table 4).



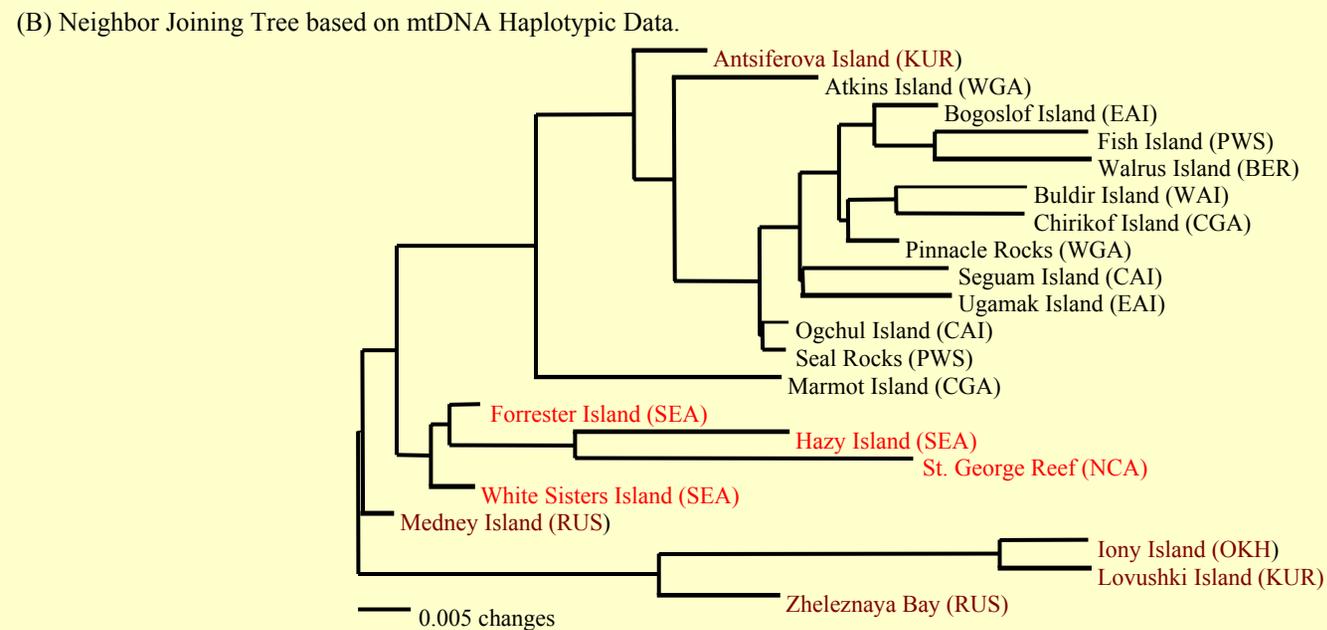
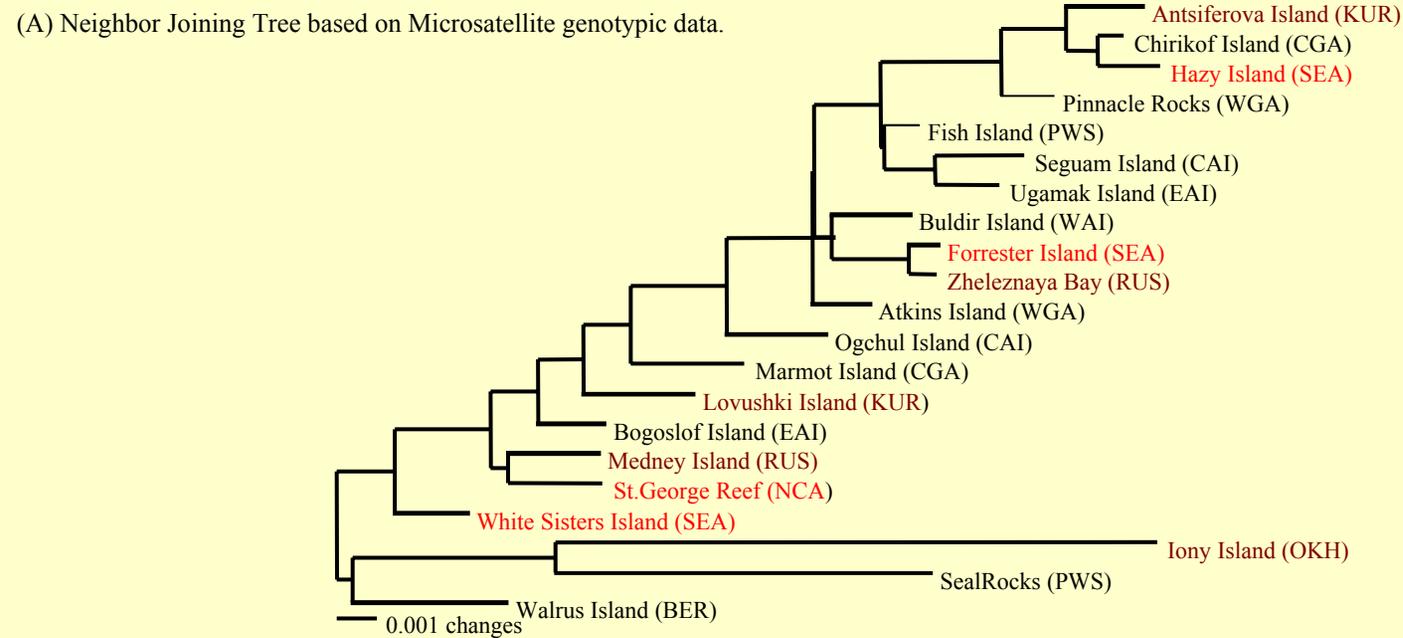


Figure 2: Neighbor Joining Trees based on Slatkin's Linearized Fst at the Rookery Level. Regional designations in parenthesis. (OKH = Sea of Okhotsk; KUR = Kuril Islands; RUS = Russia; WAI = Western Aleutian Islands; CAI = Central Aleutian Islands; EAI = Eastern Aleutian Islands; BER = Bering Sea; WGA = Western Gulf of Alaska; CGA = Central Gulf of Alaska; PWS = Prince William

